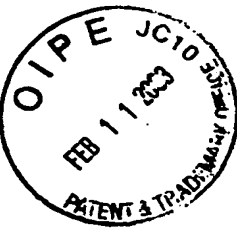


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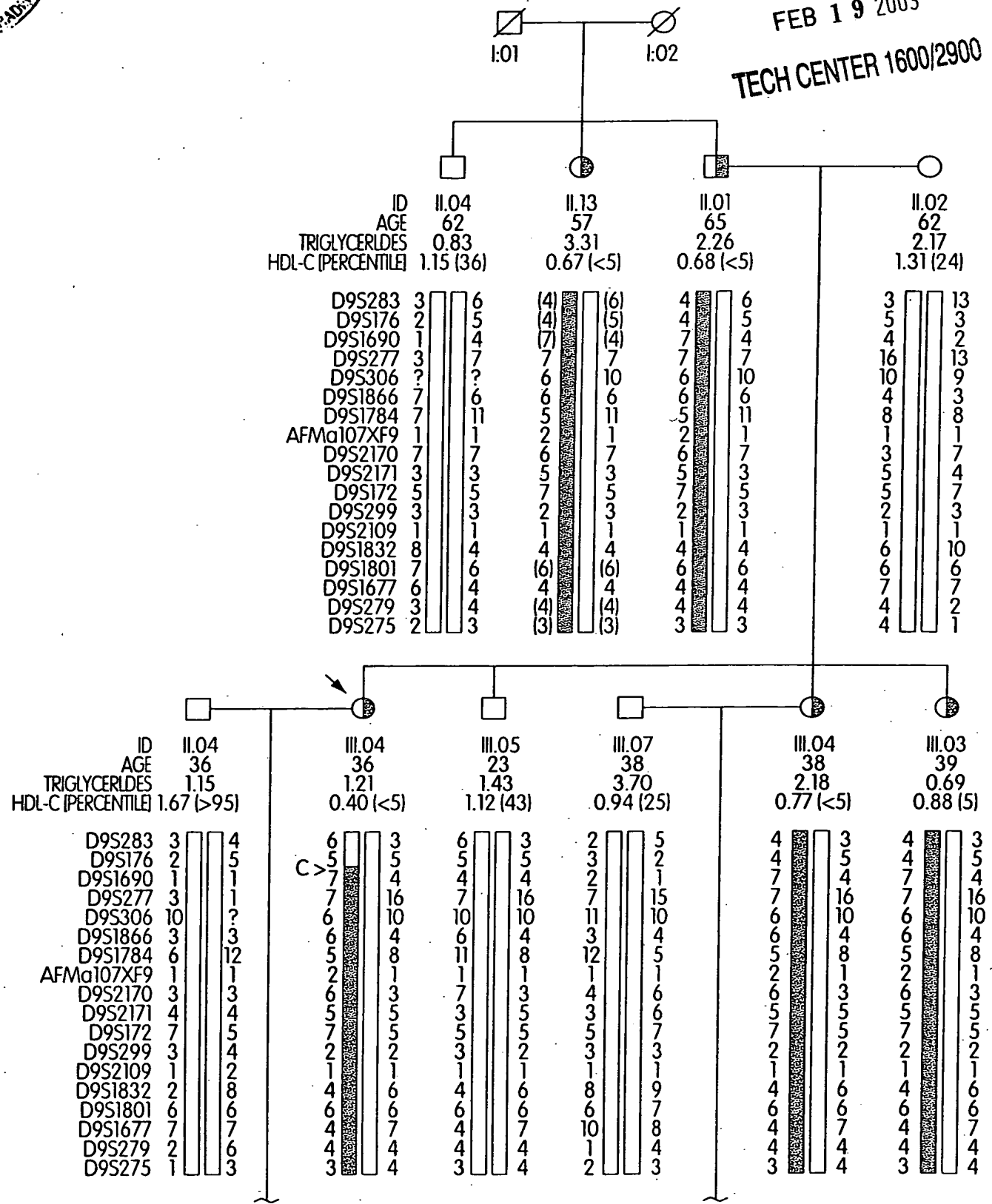
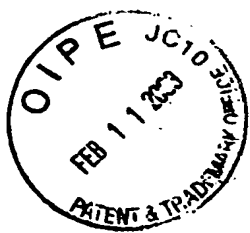


Figure 2A – (1)



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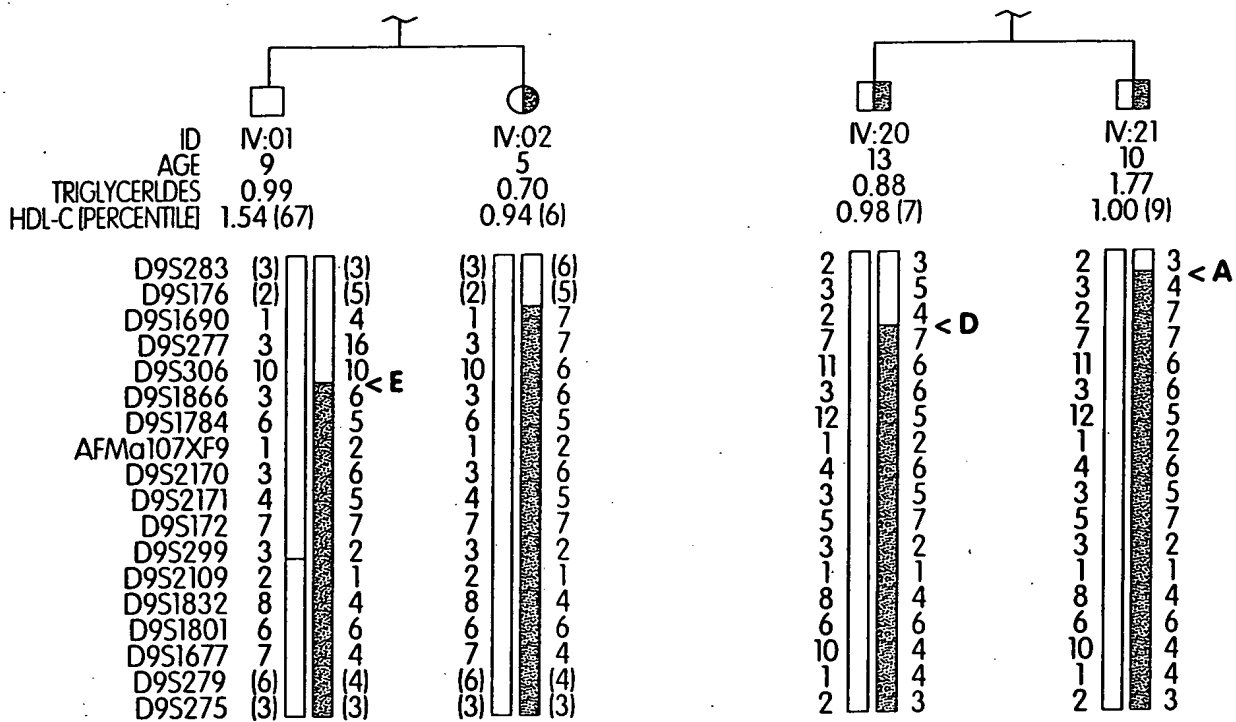
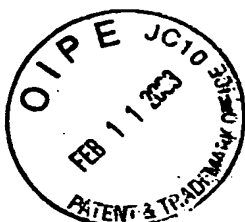


Figure 2A – (2)



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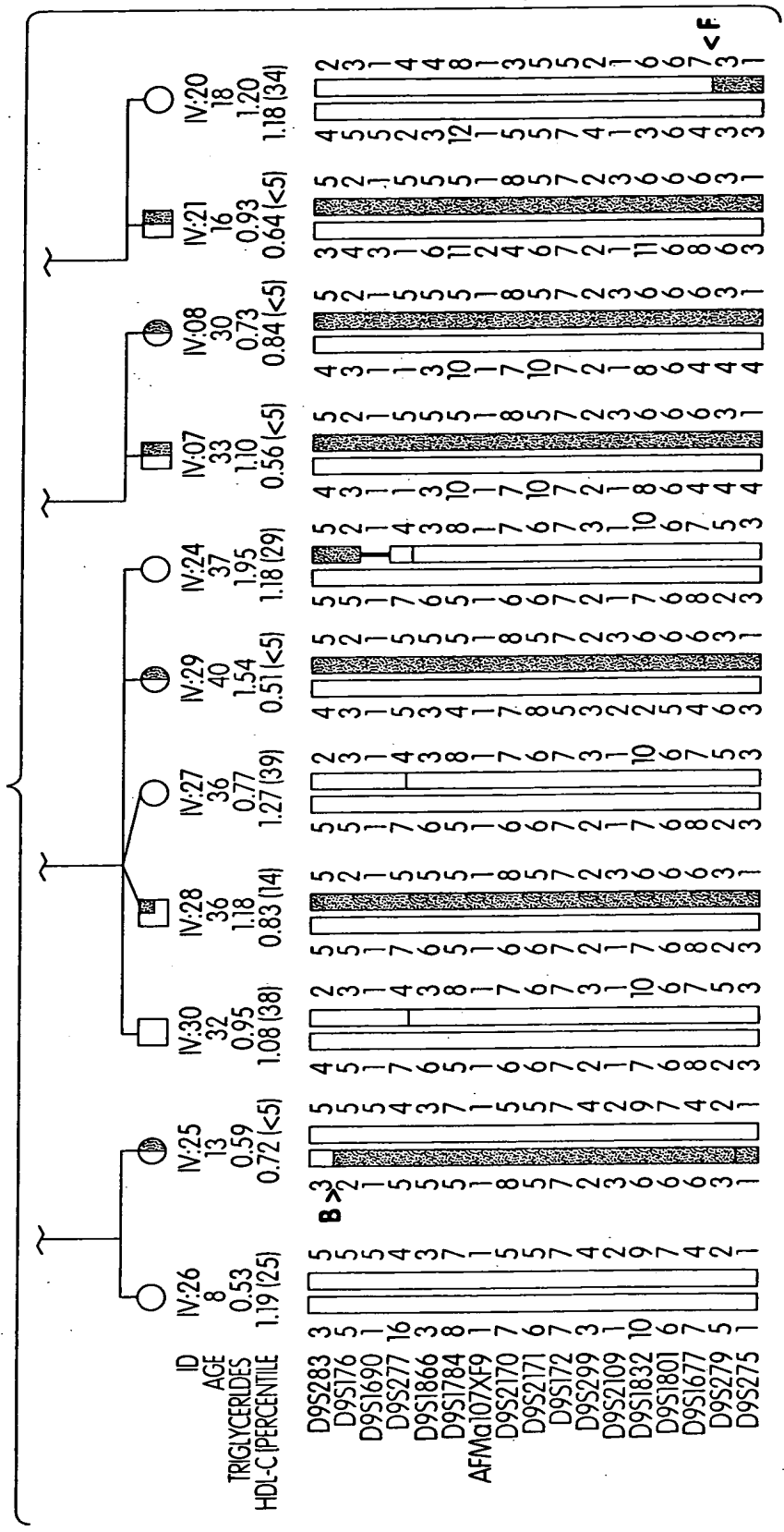


Figure 2B - (2)



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Exon	Exon Forward Primer (bp)	SEQ ID No.	Reverse Primer	SEQ ID No.	intron	intron(kb)	intron (kb)
1	140 GGCTGGATTAGCAGTCTCTCA	70	ATCCCAACTCAAAACCACA	119	intron 1	>6.413	>6.413
exon 2	94 GGATTTCACAGATCCAGTG	71	AAGTCCAAATTAGCCACGTT	120	intron 2	>4.241	>4.241
exon 3	142 GACAGACTTGGCATGAAGCA	72	CCAGCCATTCAAAATTCCTCC	121	intron 3	>1.248(1.6)	>1.248(1.6)
exon 4	119 GCACAGACTTGGCATGAAGCA	73	GGGTGCAAGTCAATTTCCAAT	122	intron 4	>1.512	>1.512
exon 5	122 CGATTTCACAGTCTCTCTCTG	74	CCCTTCAACCACTTACAA	123	intron 5	>1.796(3)	>1.796(3)
exon 6	177 ACTTCAAGGACCCAGCTTCC	75	TGTCCAGGAAAGCCCTCAC	124	intron 6	>2.726 (10)	>2.726 (10)
exon 7	93 TCGGTTTCTTGTGTTTAAACTCA	76	AGGACCTCTGCCAGACTCA	125	intron 7	4.975	4.975
exon 8	241 TCCCAAGGCTTTGAGATGAC	77	AGGAGATGACACAGGCCAAG	126	intron 8	>2.311(.5)	>2.311(.5)
exon 9	140 GGTCCAAAGCCCTTGTAA	78	CGCACCTCTGAAGCTACC	127	intron 9	0.332	0.332
exon 10	117 GCTGCTGTGATGGGTATCT	79	ACCTCACTCACACCTGGGA	128	intron 10	4.208	4.208
exon 11	198 TTGTAAATTTGTAGTGTCTCTCA	80	GCCTCCTGCTGAACCTTAT	129	intron 11	0.747	0.747
exon 12	206 TAGTCAGCCCTTGCCCTCTA	81	CAAAATCATGACACCAAGTTGAG	130	intron 12	0.523	0.523
exon 13	177 AAAGGGCTTGGTAAGGTA	82	CATGCACATGACACACATA	131	intron 13	1.787	1.787
exon 14	223 GATGTGTGCTCCCTCTAGC	83	CCTTAGCCCGTTTGAGCTA	132	intron 14	1.747	1.747
exon 15	222 CAAGTGAAGTCTTGGGATTG	84	TGCTTTTATTCAGGACTCCA	133	intron 15	1.059	1.059
exon 16	205 GCAATTCAAATTTCTCCAGG	85	CCCATGCACATGACAGATTC	134	intron 16	1.105	1.105
exon 17	114 TCAAGGAGGAATGGACCTG	86	AAGCAGGAGACATCGCTT	135	intron 17	1.789	1.789
exon 18	172 CTGAAGTTCAAGCGCAGTG	87	GGGATCAGCATGCTTTCCTA	136	intron 18	0.99	0.99
exon 19	132 TGCAGATGAATGGAGCATC	88	GCTTAAGTCCCACTCTCTCCC	137	intron 19	1.307	1.307
exon 20	143 GCCAGGGACACTGTATTCT	89	ATTTTCTCTCCGATGTGT	138	intron 20	0.204	0.204
exon 21	138 AGGTCTCTGCTTCACTCA	90	TCACAGAAGCCTAGCCATGA	139	intron 21	0.706	0.706
exon 22	221 CCAGTGTCTACCCCTGCTAA	91	AACAGAGCAGGAGATGGTG	140	intron 22	>0.866(1.7)	>0.866(1.7)
exon 23	73 CACACACAGAGCTTCTTGGG	92	TCTGCACTCTCTCTCTCTG	141	intron 23	0.986	0.986
exon 24	203 ACCTGGACAGGTGTGGTGT	93	ACTGGGGCAACATTAATCA	142	intron 24	1.668	1.668
exon 25	49 GGGCTAACATGCCACTCAGTA	94	CTTCCCATCTGCAACAAC	143	intron 25	0.196	0.196

Figure 10A



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exon 26	114	GTCTGTTGCAGATGGGGAAG	144	GCTAAGGGCCATCCAAAGAA	intron 26	306	1.396	1.4
exon 27	149	CACCAGAAGAGGACATGG	145	TCAGTGCATCTGGGCATAA	intron 27	307	1.649	1.6
exon 28	125	CTGGACTCGTAGGATTTGC	146	TCCTGAAGTCCATTCCTTGG	intron 28	308	>0.728(1.4)	1.4
exon 29	99	GCCTGTACAGAGAAATGCTT	147	CAATGTGGCATGCAGTTGAT	intron 29	309	>2.589(3)	3
exon 30	190	TTACGGATGATCCTGTGCTC	148	GAAGTACCAGCCCATCCT	intron 30	310	1.521	1.5
exon 31	95	AGTCAGGTTCCGGTCACAC	149	CATTCCCCCAGTGTTCAG	intron 31	311	>0.944(1)	>0.9
exon 32	33	CCGTTCCCTATATCCTCAGTG	150	CCAAGGCTTCTTCAATCCA	intron 32	312	>1.062(/6.5)	>1.0
exon 33	106	CCTGTACACACTCGCACTGA	151	GATCGTTTAACTTCCCAAC	intron 33	313	1.475	1.5
exon 34	75	TGTTGTCCACAGGTTCCAGA	152	ATGCCCTGCCAACTTAC	intron 34	314	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	153	CTCTGAGCTGTTCCTTAC	intron 35	315	1.228	1.2
exon 36	178	ATGTTTTCCTTGGCTGTGC	154	TATCAATCCATGGCCCTGAC	intron 36	316	>1.898(2)	2
exon 37	116	ATCTGCCCTTCTTGTCTGA	155	AGAGTCCCTGCCCTCCTTCT	intron 37	317	0.112	0.1
exon 38	145	AGGAGCTGCACAGTGGATA	156	AAGGCAGTCAGCAGTCAAA	intron 38	318	1.545	1.5
exon 39	124	TCACCTCCCATATTTTCAGACTTGA	157	GGGGAACATCTGTGCTTAG	intron 39	319	1.087	1.1
exon 40	130	TGTTTATTTGGAAGATCGGTGA	158	CCATTGGTGAGTGTTCCTT	intron 40	320	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCTG	159	AGTCAGCAAACTGCTGGGTT	intron 41	321	>0.622(0.9)	0.9
exon 42	63	AGTCCTGCCCTTCCACAGTTG	160	ATTGCTCCATCCTGGCATAA	intron 42	322	0.909	0.9
exon 43	107	GGTAGTTACGTGTAGGGGCA	161	TCATGGATGATTTTATGTGCTTC	intron 43	323	2.355	2.4
exon 44	142	CAGGAACATTAGGCCAGATTG	162	GCGTGTGGAAGGCCATAAG	intron 44	324	0.372	0.4
exon 45	135	CATGTATGTGTAGGACAGCATGA	163	GCCATCATACACACGCCCT	intron 45	325	>1.059(1.3)	1.3
exon 46	104	CTGTTTCAAGATGCTTCTGC	164	TGATCGCATATTTCTACTTGGAAA	intron 46	326	0.483	0.5
exon 47	93	CCTAGGAAGCTGGAATGCTG	165	TCCCTTTATTTTAGAGGCACCA	intron 47	327	0.659	0.7
exon 48	244	GGGTTCCACAGGTTTCAGTAT	166	GATCAGGAATTCAGGCACCAA	intron 48	328	0.941	0.9
exon 49	295	CTTGACCTAATTTCAACATCTGG	167	TGGGTTCCATAATAGAGTTTCA			>1.075	

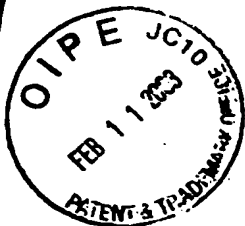
Figure 10B

ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):				
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
2	T150C A152G	no change	Public sequence: TGTGAGCTGTACTGGAAGTGG Correct sequence: TGTGAGCTGTCTGGAAGTGG	168 169
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGCCACAA Correct sequence: AGGAGCTGGCTGAAGCCACAA	170 171
33	C4738T	T1495I	Public sequence: AATGATGCCACCAAAACAATG Correct sequence: AATGATGCCATCAAAACAATG	172 173
35	C5017T	P1588L	Public sequence: GAGGTGGCTCCGATGACCACA Correct sequence: GAGGTGGCTCTGATGACCACA	174 175
43	G5995A	R1914K	Public sequence: TTCCTTAACAGAAATAGTATC Correct sequence: TTCCTTAACAAAATAGTATC	176 177
48	C6577T	P2108L	Public sequence: GGAAGTGTCCAAAAGAGAAA Correct sequence: GGAAGTGTCTAAAAGAGAAA	178 179
49	G6899A	not applicable	Public sequence: AGTAAAGAGGACTAGACTTT Correct sequence: AGTAAAGAGCAACTAGACTTT	180 181
Mutations:				
13	A1864G	Q597R	More common: GCCTACTTGCAGGATGTGGTG Less common: GCCTACTTGGCGGATGTGGTG	182 183
14	delta CTT 2151-3	delta L093	More common: CCTCATTCCTCTTCTTGAGCGG Less common: CCTCATTCCT/CTTGAGCGG	184 185
15	G2385A	V771M	More common: GCAGGACTACGTGGGCTTCAC Less common: GCAGGACTACATGGGCTTCAC	186 187
18	C2799T	R909Stop	More common: AAAAGTCTACCGAGATGGAT Less common: AAAAGTCTACTGAGATGGAT	188 189
18	C2860T	T929I	More common: GGCCAGATCACCTCCCTTCCTG Less common: GGCCAGATCATCTCCCTTCCTG	190 191
22	T3346C	M1091T	More common: ACACACCATGGATGAGCG Less common: ACACACCATCGGATGAGCG	192 193

Figure 11A

Intron 24	(+1) G to C splice donor site	Altered transcript length	More common: Less common:	CCTGGAAGAGTAAGTTAAGT CCTGGAAGACTAAGTTAAGT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCCTGTGTCTCCCCAGG GCTGCCCTGTGCGTCCCCAGG	196 197
35	GG 4958-57 to C	frameshift at aa 1628	More common: Less common:	TAGCCATTATGGAATTAAGTCT TAGCCATTATCAATTAAGTCT	198 199
41	delta AAGATG 5752-7	delta (E.D) 1893-1894	More common: Less common:	GATGAAGATGAAGATGTGAGCGGGGA GATGAAGATG/TGAGCGGGGA	200 201
48	C6504T	R2144Stop	More common: Less common:	AATAGTTGTAGGAATAGCAGG AATAGTTGTATGAATAGCAGG	202 203
Promoter Variants: Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common: Less common:	ACACGCTGGGGGTCTGGCTG ACACGCTGGGGGTCTGGCTG	204 205
5	(-)4 ins. G	8158	More common: Less common:	GACACGCCACGGGTCTCCCTG GACACGCCACGGGTCTCCCTG	206 207
5	A (-)380 G	7780	More common: Less common:	CATTTCCTTAGAAAAGAGAGGT CATTTCCTTAGAAAAGAGAGGT	208 209
5	A (-)479 C	7681	More common: Less common:	GAAATTAGTATGTAAGGAAG GAAATTAGTCTGTAAGGAAG	210 211
5	A (-)738 G	7422	More common: Less common:	CCTCGGCTGCCAGGTTTCAGCGATT CCTCGGCTGCCAGGTTTCAGCGATT	212 213
5	A (-)1045 G	7115	More common: Less common:	TATGTGCTGACCATGGGAGCTTGT TATGTGCTGACCGTGGGAGCTTGT	214 215
5	A (-)1113 G	7047	More common: Less common:	GTGACACCCAAACGAGTAGGG GTGACACCCGAGCGGAGTAGGG	216 217
5	(-)1181 ins. CCCT	6979	More common: Less common:	AGTATCCCT/TGTTACCGAGAA AGTATCCCTCCCTGTTTCACGAGAA	218 219

Figure 11B



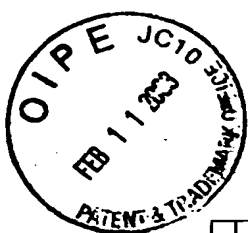
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Polymorphisms:					
Exon/Intron	Nucleotides	Amino Acid Change		Sequence difference/context	SEQ ID NO:
5	G548A	no change	More common:	CTGGGTTCTGTATCACAACC	220
			Less common:	CTGGGTTCTATATCACAACC	221
6	G730A	R219K	More common:	GGCCTACCAAGGGAGAACTG	222
			Less common:	GGCCTACCAAGGAGAACTG	223
Intron 7	G(+2383 T	Not applicable	Allele 1:	TTTAAAGGGGTGATTAGGA	224
			Allele 2:	TTTAAAGGGGTGATTAGGA	225
Intron 7	G(+3035 T	Not applicable	Allele 1:	GAAGAAATTTGTTTTTTTGATT	226
			Allele 2:	GAAGAAATTTTTTTTTTGATT	227
8	C1010T	no change	More common:	GCGGGCATCCCGAGGAGGGG	228
			Less common:	GCGGGCATCTTGAGGAGGGG	229
8	G1022A	no change	More common:	AGGAGGGGGCTGAAGATCA	230
			Less common:	AGGAGGGGGACTGAAGATCA	231
Intron 9	(-)42 ins. G	Not applicable	More common:	AGGAGCCAAACGGCTCATTTGT	232
			Less common:	AGGAGCCAAAGCGCTCATTTGT	233
Intron 13	T(+24 A	Not applicable	More common:	AAGCCACTGTTTTTAAACCAGT	234
			Less common:	AAGCCACTGTATTTAAACCAGT	235
15	A2394C	T774P	More common:	CGTGGGCTTCACACTCAAGAT	236
			Less common:	CGTGGGCTTCCCACTCAAGAT	237
15	G2402C	K776N	More common:	TCACACTCAAGATCTTCGCTG	238
			Less common:	TCACACTCAACATCTTCGCTG	239
Intron 14	C(+16 T	Not applicable	Allele 1:	GCAGCCTCACCGGCTCTTCCC	240
			Allele 2:	GCAGCCTCACTCGGCTCTTCCC	241
17	A2723G	I883M	Allele 1:	AGAAGAGAAATATCAGAAATCT	242
			Allele 2:	AGAAGAGAAATCTCAGAAATCT	243
Intron 17	C(+2000 G	Not applicable	Allele 1:	GCCGAGTGCCTGTGTCTTTA	244
			Allele 2:	GCCGAGTGCCTGTGTCTTTA	245

Figure 11C



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21	T3233G	no change	More common: Less common:	GATCTAAGGTTGTCATCTCTGG GATCTAAGGTTGTCATCTCTGG	246 247
Intron 21	G(+118 T	Not applicable	Allele 1: Allele 2:	CTCTTCCTGTTAGGACAGAAGAGA CTCTTCCTGTTATCAGAAGAGA	248 249
Intron 21	A(+1563 G	Not applicable	Allele 1: Allele 2:	CATTCTAGGGATCATAGCCAT CATTCTAGGGGTCATAGCCAT	250 251
Intron 24	G(+1321 T	Not applicable	Allele 1: Allele 2:	AAGTACAGTGGGAGAACACGG AAGTACAGTGTGAGAACACGG	252 253
Intron 29	A(-1624 G	Not applicable	Allele 1: Allele 2:	AATTCCTAATAAATAGAAATGCA ATTCTTAATAAAGTAGAAATGCA	254 255
Intron 31	T(+130 C	Not applicable	More common: Less common:	GGCCCCCTGCTTATTTACT GGCCCCCTGCTTATTTACT	256 257
Intron 33	A(+1732 G	Not applicable	Allele 1: Allele 2:	TGAGAGATTTACTTGAACCCGG TGAGAGATTTGCTTGAACCCGG	258 259
Intron 33	C(+1898 T	Not applicable	Allele 1: Allele 2:	TTTGCTGAACAATCACTGCA TTTGCTGAATAATCACTGAC	260 261
Intron 34	C(+1234 T	Not applicable	Allele 1: Allele 2:	AACCTCAGTCCCTCACTGTC AACCTCAGTTCCTCATCTGTC	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACAGAAATATGTC CTGGACACCAAAATATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGTCCTCCACCAAT TCCTATGTCCTCCACCAAT	266 267
Intron 43	T(+118 C	Not applicable	More common: Less common:	AAGAAGTGGCTGTATTTTC AAGAAGTGGCTGTATTTTC	268 269
Intron 43	C(+1665 G	Not applicable	Allele 1: Allele 2:	AACGTATTTGATTTGGTATAGCTG AACTGATTTGTTGGTATAGCTG	270 271
48	C6521T	no change	More common: Less common:	CAGGGTCCAAACCCGACCTGA CAGGGTCCAAATCCGACCTGA	272 273
Intron 10	(+14 ins. T	Not applicable	More common: Less common:	GGCTCAGGATCGGGACAG GGCTCAGGATCGGGACAG	284 285
Exon 16	G2547A	V8251	More common: Less common:	CCACTTCGGTCTCCATG CCACTTCGATCTCCATG	286 287
Polymorphism in an ABC1 BAC contig: This polymorphism is within approximately 200bp of the ABC1 gene					SEQ ID NO:
	A or G	Not applicable	Allele 1: Allele 2:	TTGGGAGGCTAAGGCAGGAGAA TTGGGAGGCTGAGGCAGGAGAA	274 275

Figure 11D



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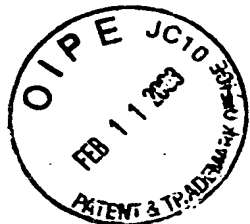
Genomic contig containing ABC1 exon 1:

Underline = putitive promotor element

acctcttatagaatgatagaattcctctggaatgattggataacttcatttcaccttgacttttaccttggaggattt
cttacccttttggcttctcaaatttgactattaaaatgttgccctttaaataaggaacacagtttcaggggggagtac
cagcccatgacccttctgcaaggcccccctaactcaaggtagttccctggaactgtggtttatggaatgttcaggagt
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Figure 12A-(1)

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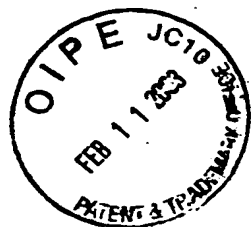
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Figure 12A-(2)



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Figure 12A-(3)

SEQ ID NO: 15

Genomic contig containing ABC1 exon 2:

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Figure 12B - (1)

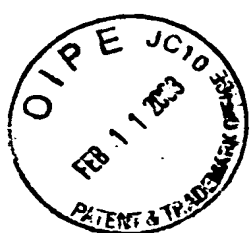


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Figure 12B - (2)



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Figure 12C - (2)



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SEQ ID NO 17

Genomic contig containing ABC1 exon 4:

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Figure 12D



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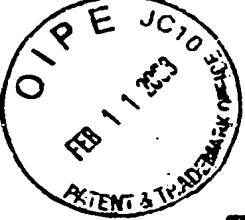
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SEQ ID NO 19

Genomic contig containing ABC1 exon 6:

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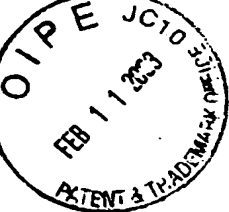
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SEQ ID NO 20

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Figure 12G - (1)



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Figure 12G - (2)



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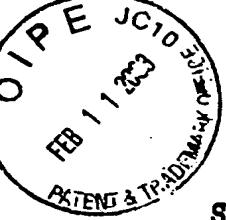
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Figure 12G - (3)



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Figure 12H - (1)

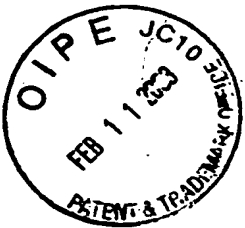


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Figure 12H - (2)



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Figure 12H - (4)



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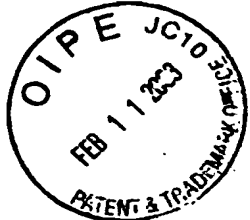
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Figure 12H - (5)



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Figure 12H - (6)

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Figure 12 I - (1)



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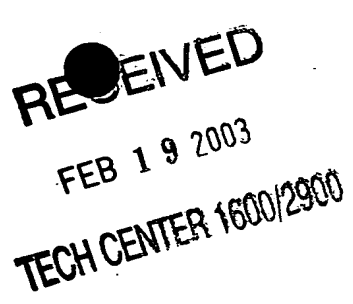
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Figure 121 - (2)



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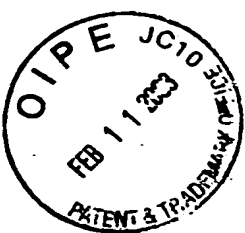
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SEQ ID NO: 24

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Figure 12K



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SEQ ID NO: 25

Genomic contig containing ABC1 exon 32: _

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Figure 12L

SEQ ID NO: 26

Genomic contig containing ABC1 exon 33 to 36:

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Figure 12M – (1)



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SEQ ID NO: 27 TECH CENTER 1600/2900 66/76

Genomic contig containing ABC1 exon 37 to 41:

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Figure 12N – (1)



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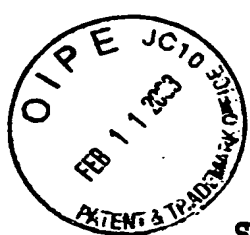
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Figure 12N – (2)



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SEQ ID NO: 28
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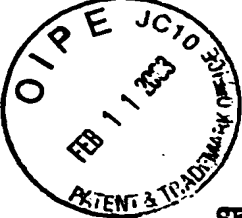
Figure 120 – (1)



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Figure 120 – (2)



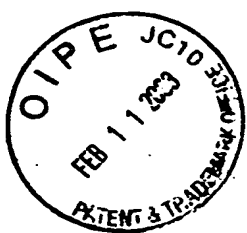
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SEQ ID NO. 29

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Figure 12P – (1)



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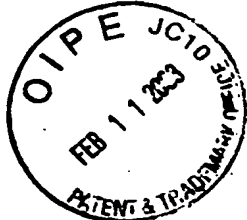
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Figure 12P – (2)

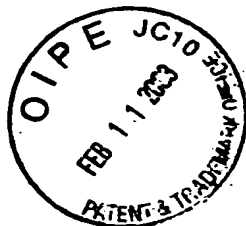


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No. Name	Location in SEQ ID No. 14	Sequence	Sequence Strand Length
1 PPPE	58-69	AGGTAAAGTCA	12 Complement
2 PPPE	1997-2009	AGAGTAGAGGGCA	13 Lead
3 PPPE	2150-2161	ATGTCAAGTTCA	12 Lead
4 PPPE	2156-2169	AGTTCAAAAGGGCA	14 Lead
5 PPPE	4126-1139	AGGCCAGCAGGGCC	14 Complement
6 PPPE	5075-5087	AGGCAGAAAGTGA	13 Lead
7 PPPE	6604-6615	ATGCCAAGGTCA	12 Complement
8 PPPE	6731-6743	GGGGCAAGGGTA	13 Complement
9 PPPE	7220-7233	AGGTAATGAGGACA	14 Complement
10 PPPE	7554-7568	GGATCACGAGGTCA	15 Complement
1 SRE	159-166	CAGCCCAT	8 Lead
2 SRE	1133-1140	CAGCTCAC	8 Complement
3 SRE	1145-1152	CACACCAC	8 Lead
4 SRE	1809-1816	CAGCCCTC	8 Complement
5 SRE	1894-1901	CAGCCCAT	8 Lead
6 SRE	2563-2570	CAACCAC	8 Lead
7 SRE	3303-3310	CAGCTCAC	8 Lead
8 SRE	3470-3477	CCGCCAC	8 Lead
9 SRE	4784-4791	CTCCAC	8 Complement
10 SRE	4802-4809	CAGCTTAC	8 Complement
11 SRE	4970-4977	CACCTCAC	8 Complement
12 SRE	6487-6494	CAGCTTAC	8 Complement
13 SRE	6565-6572	CACCCAAC	8 Complement
14 SRE	6727-6734	CACCTTCA	8 Lead
15 SRE	7041-7048	CACCCAAC	8 Lead
16 SRE	8059-8066	CAGCCCTC	8 Complement
1 ROR (retinoic acid receptor related)	166-172	AGGTCA	7 Complement
2 ROR (retinoic acid receptor related)	166-173	AAGGTCA	8 Complement
3 ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8 Lead
4 ROR (retinoic acid receptor related)	264-370	TGGGTCA	7 Lead
5 ROR (retinoic acid receptor related)	2218-2225	TAGGTCA	8 Lead
6 ROR (retinoic acid receptor related)	2219-2225	AGGTCA	8 Lead
7 ROR (retinoic acid receptor related)	3643-2649	TGGGTCA	7 Lead
8 ROR (retinoic acid receptor related)	6604-6610	AAGGTCA	7 Complement
1 SREBP-1 or "E box"	473-479	ACACCTG	7 Complement
2 SREBP-1 or "E box"	536-541	ACACATG	7 Lead
3 SREBP-1 or "E box"	537-543	TCATGTG	7 Complement
4 SREBP-1 or "E box"	655-661	TCATGTG	7 Complement
5 SREBP-1 or "E box"	925-931	ACACTTG	7 Lead
6 SREBP-1 or "E box"	967-973	TCACTTG	7 Lead
7 SREBP-1 or "E box"	968-974	TCAAGTG	7 Complement
8 SREBP-1 or "E box"	1053-1069	ACAGGTG	7 Complement
9 SREBP-1 or "E box"	1104-1110	TCACTTG	7 Lead
10 SREBP-1 or "E box"	1105-1111	TCAAGTG	7 Complement
11 SREBP-1 or "E box"	1561-1567	TCACTTG	7 Lead

Figure 16A



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12	SREBP-1	or	"E box"	1670-1676	TCAAATG	Lead	7
13	SREBP-1	or	"E box"	1748-1754	ACACTTG	Lead	7
14	SREBP-1	or	"E box"	1749-1755	ACAAAGT	Complement	7
15	SREBP-1	or	"E box"	1852-1858	TCATGTG	Lead	7
16	SREBP-1	or	"E box"	1853-1859	ACACATG	Complement	7
17	SREBP-1	or	"E box"	1899-1905	ACAAATG	Complement	7
18	SREBP-1	or	"E box"	2199-2205	ACACGTG	Lead	7
19	SREBP-1	or	"E box"	2393-2399	ACAGCTG	Complement	7
20	SREBP-1	or	"E box"	2669-27005	ACACCTG	Lead	7
21	SREBP-1	or	"E box"	2677-2683	TCACATG	Complement	7
22	SREBP-1	or	"E box"	2740-2746	ACAAATG	Complement	7
23	SREBP-1	or	"E box"	2969-2975	ACAAATG	Complement	7
24	SREBP-1	or	"E box"	2979-2985	ACACATG	Lead	7
25	SREBP-1	or	"E box"	2981-2987	ACATGTG	Lead	7
26	SREBP-1	or	"E box"	2980-2986	ACATGTG	Lead	7
27	SREBP-1	or	"E box"	2982-2988	ACATGTG	Complement	7
28	SREBP-1	or	"E box"	3461-3467	TCAGGTG	Complement	7
29	SREBP-1	or	"E box"	3462-2468	TCACCTG	Lead	7
30	SREBP-1	or	"E box"	3547-3553	TCACCTG	Complement	7
31	SREBP-1	or	"E box"	3752-3758	TCACATG	Complement	7
32	SREBP-1	or	"E box"	4226-4232	TCACCTG	Lead	7
33	SREBP-1	or	"E box"	4582-4588	ACACGTG	Complement	7
34	SREBP-1	or	"E box"	4588-4594	TCAGGTG	Lead	7
35	SREBP-1	or	"E box"	4861-4867	TCAGGTG	Lead	7
36	SREBP-1	or	"E box"	4951-4957	ACAAATG	Lead	7
37	SREBP-1	or	"E box"	5096-5102	TCAAATG	Complement	7
38	SREBP-1	or	"E box"	5912-5918	ACAGTGT	Lead	7
39	SREBP-1	or	"E box"	5913-5919	TCACCTG	Complement	7
40	SREBP-1	or	"E box"	6245-6251	ACACATG	Complement	7
41	SREBP-1	or	"E box"	6288-6294	ACAAATG	Complement	7
42	SREBP-1	or	"E box"	6623-6629	TCATTGT	Lead	7
43	SREBP-1	or	"E box"	6836-6842	TCACCTG	Lead	7
44	SREBP-1	or	"E box"	6837-6843	ACAGGTG	Complement	7
45	SREBP-1	or	"E box"	7032-7038	ACAGGTG	Complement	7
46	SREBP-1	or	"E box"	7069-7075	TCAGGTG	Lead	7
47	SREBP-1	or	"E box"	7101-7107	ACATATG	Complement	7
48	SREBP-1	or	"E box"	7138-7144	ACAGTGT	Lead	7
49	SREBP-1	or	"E box"	7139-7145	TCACCTG	Complement	7
50	SREBP-1	or	"E box"	7240-7246	ACACCTG	Complement	7
51	SREBP-1	or	"E box"	7467-7473	ACAGGTG	Lead	7
52	SREBP-1	or	"E box"	7640-7646	TCATTGT	Lead	7
53	SREBP-1	or	"E box"	7641-7647	TCAAATG	Complement	7
54	SREBP-1	or	"E box"	7653-7659	TCACCTG	Lead	7
55	SREBP-1	or	"E box"	7654-7660	ACAAATG	Complement	7
56	SREBP-1	or	"E box"	7735-7741	ACAAATG	Lead	7
57	SREBP-1	or	"E box"	7838-7844	TCAGGTG	Complement	7
58	SREBP-1	or	"E box"	7880-7886	TCATCTG	Complement	7
59	SREBP-1	or	"E box"	8051-8057	TCAGCTG	Lead	7
60	SREBP-1	or	"E box"	8052-8058	TCAGCTG	Complement	7

Figure 16B